

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Currently amended) A method for detecting a candidate substance comprising the steps of:

(a) incubating a test substance with a biomolecule selected from group I, wherein group I consists of the protein BNPI or DNPI or a protein comprising SEQ ID NO: 2, 4, 6, 8, 10, 12 or 14 ~~or a protein which is at least 90% homologous thereto~~ or a protein encoded by a polynucleotide comprising SEQ ID NO: 1, 3, 5, 7, 9, 11 or 13 or a polynucleotide which is at least 90% homologous thereto, or antisense polynucleotides thereof, ~~or a part protein of one of the abovementioned proteins which is at least 10 amino acids long~~ or a cell or a preparation from a cell which has synthesized at least one of the abovementioned proteins ~~or part proteins~~

(b) measuring the binding of the test substance to the protein ~~or part protein~~ or the protein ~~or part protein~~ synthesized by the cell ~~or measuring at least one functional parameter modified by the binding of the test substance to the protein or part protein wherein measuring said functional parameter involves measuring the regulation, inhibition or activation of receptors, ion channels or enzymes or via measurement of a modification in gene expression, pH or membrane potential, or via a modification in enzyme activity or concentration of a second messenger and~~

(c) determining whether the test substance is a pain-relevant substance.

2. (Previously presented) A method according to claim 1, wherein the cell is manipulated by genetic engineering before step (a) said genetic engineering comprising introducing genetic material into said cell.
3. (Original) A method according to claim 2, wherein the manipulation by genetic engineering allows the measurement of at least one functional parameter modified by the binding of the test substance.
4. (Canceled)
5. (Withdrawn) A method according to claim 2, wherein the cell is manipulated by genetic engineering so that the cell contains at least one polynucleotide selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11 and 13, or a polynucleotide which is at least 90% homologous thereto.
6. (Withdrawn) A method according to claim 5, wherein the polynucleotide is contained in a recombinant DNA construct.
7. (Original) A method according to claim 2, wherein after the manipulation by genetic engineering according to claim 2 and before step (a), the cell is cultured under conditions which allow expression.
8. (Original) A method according to claim 7, wherein the cell is cultured under selection pressure.
9. (Previously presented) A method according to claim 1, wherein the cell is an amphibia cell, bacteria cell, yeast cell, insect cell or an immortalized mammalian cell.
10. (Original) A method according to claim 1, wherein the measurement of the binding is carried out via the displacement of a known labeled ligand of the part protein or protein or via the activity bound thereto from a labeled test substance.

11. (Canceled)

12. (Canceled)

13. (Withdrawn) A method according to claim 1, in which a first method according to claim 1 is coupled with a second method according to claim 1 such that the measurement values and results of the first method in respect of the substance to be measured are compared with the measurement values and results of the second method in respect of the substance to be measured, wherein one of the two methods is the main method, wherein, in step (a) of said main method, the substance to be tested is incubated

either

with a biomolecule selected from group II, wherein group II consists of the the protein BNPI or a protein comprising SEQ ID NO: 2, 4, 6 or 8 or a protein which is at least 90% homologous thereto or a protein encoded by a polynucleotide comprising SEQ ID NO: 1, 3, 5 or 7 or a polynucleotide which is at least 90% homologous thereto, or a protein encoded by a nucleic acid which is the reverse complement of a polynucleotide comprising SEQ ID NO: 1, 3, 5 or 7 or antisense polynucleotides thereof, or a part protein of one of the abovementioned proteins which is at least 10 amino acids long or a cell or a preparation from a cell which has synthesized at least one of the abovementioned proteins or part proteins,

or

with a biomolecule selected from group III, wherein group III consists of the protein DNPI or a protein comprising SEQ ID NO: 10, 12 or 14, or a protein which at least 90% homologous thereto or a protein encoded by a polynucleotide comprising SEQ ID NO: 9, 11 or 13 or a polynucleotide which is at least 90% homologous thereto, or a protein encoded by a nucleic acid which is the reverse complement of a polynucleotide comprising SEQ ID NO: 9, 11 or 13 or antisense

polynucleotides thereof, or a part protein of one of the abovementioned proteins which is at least 10 amino acids long or a cell or a preparation from a cell which has synthesized at least one of the abovementioned proteins or part proteins,
and

wherein, in a secondary method, in step (a) the substance to be tested is incubated with a biomolecule from group I or with a biomolecule selected from group II or group III, wherein the biomolecule selected from group II or group III is selected from a group which differs from group the biomolecule with which the substance in the main method is incubated.

14. (Previously presented) A method according to claim 1, wherein the pain regulated by the substance to be detected is selected from the group consisting of: chronic pain, neuropathic pain, mechanical hyperalgesia, diabetic neuropathy; visceral pain, cerebral pain, peripheral pain, inflammation-related pain, migraine, cluster headache and pain with trigeminus neuralgia.

15. (Original) The method of claim 14, wherein said pain is either musculoskeletal pain, allodynic pain or peripheral inflammation pain.

16-32. (Canceled)

33. (New) The method of claim 1, wherein the step of determining whether the test substance is a pain-relevant substance includes testing the test substance for pain relevance in an animal model.